Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently amended) Method for identifying cytosine methylation patterns in genomic DNA samples, said method comprising the steps of:

a) chemically treating a genomic DNA sample in such a way that cytosine and 5-methylcytosine react differently and a different base pairing behavior of the two products is obtained in the duplex;

b) enzymatically amplifying portions of the thus-treated DNA sample <u>nonspecifically with regard to methylation of said genomic DNA sample</u>;

c) binding the amplified portions of the thus-treated DNA sample to a surface;

d) contacting a set of probes of different nucleobase sequences, each of which contains the dinucleotide sequence 5'-CpG-3' at least once, to the immobilized DNA samples for hybridization <u>to distinguish methylated and nonmethylated cytosines in said genomic DNA sample</u>;

e) removing any non-hybridized probes from the immobilized DNA samples;

f) analyzing the hybridized probes in a mass spectrometer, wherein the position of the hybridized probes on the surface permits a classification of the immobilized DNA sample hybridized thereto;

g) assigning a peak pattern obtained from the mass spectra to a methylation pattern for the immobilized DNA and comparing the peak pattern with a database to identify cytosine methylation patterns in the genomic DNA sample.

2. (Original) Method according to claim 1, further characterized in that one or more amplified genomic DNA fragments are immobilized in c) by hybridization with complementary oligonucleotide or PNA sequences, which are covalently bound to the surface.

3. (Original) Method according to claim 2, further characterized in that a cross-linking of the genomic DNA fragments with the oligonucleotide or PNA sequences bound to the surface results after the hybridization.

4. (Original) Method according to claim 3, further characterized in that covalent chemical bonds are formed for the cross-linking.

5. (Original) Method according to claim 3, further characterized in that electrostatic interactions are formed for the cross-linking.

6. (Previously presented) Method according to claim 3, further characterized in that the oligonucleotide or PNA sequences bound to the surface contain 5-bromouracil structural units.

7. (Previously presented) Method according to claim 1, further characterized in that the immobilized complementary oligonucleotide sequences contain modified bases, ribose or backbone units.

8. (Previously presented) Method according to claim 1, further characterized in that the genomic DNA sample is propagated in b) in the form of several amplified fragments, so that at least 0.01% of the total genome is amplified.

9. (Previously presented) Method according to claim 1, further characterized in that the mixture of amplified DNA fragments is bound to a surface, on which a multiple number of different points is arranged, each of which can bind different portions of the amplified DNA sample.

10. (Previously presented) Method according to claim 1, further characterized in that a set of probes is used in d), which contains the dinucleotide sequence 5'-CpG-3' only once in each probe and the probes otherwise contain either no cytosine or no guanine bases.

11. (Previously presented) Method according to claim 1, further characterized in that a bisulfite or pyrosulfite or disulfite solution or a mixture of the indicated solutions is used together with other reagents for the specific or sufficiently selective conversion of cytosine to uracil.

12. (Previously presented) Method according to claim 1, further characterized in that the surface used for the immobilization of amplified sample DNA is also the sample holder for a mass spectrometer.

13. (Previously presented) Method according to claim 1, further characterized in that the surface used for the immobilization of amplified sample DNA is introduced as a whole, prior to f), onto a sample holder for a mass spectrometer.

14. (Previously presented) Method according to claim 1, further characterized in that the hybridized probes are stripped from the immobilized amplified DNA samples before, after or by contact with a matrix.

15. (Previously presented) Method according to claim 1, further characterized in that the probes are nucleic acids, which bear one or more mass tags.

16. (Original) Method according to claim 15, further characterized in that one or more mass tags are also charge tags.

17. (Original) Method according to claim 15, further characterized in that the probes also bear a charge tag.

18. (Previously presented) Method according to claim 1, further characterized in that the probes are modified nucleic acid molecules.

19. (Previously presented) Method according to claim 20, further characterized in that nucleic acid molecules are selected from the group consisting of PNAs, alkylated phosphorothioate nucleic acids and alkyl phosphonate nucleic acids.

20. (Previously presented) Method according to claim 1, further characterized in that the probes are prepared by combinatory synthesis.

21. (Currently amended) Method according to claim 20, further characterized in that different base structural units are labeled in such a way that ~~the~~ each of the probes synthesized from them can be distinguished by their mass in the mass spectrometer.

22. (Previously presented) Method according to claim 1, further characterized in that the probes are prepared as sublibraries and these are provided with different mass and/or charge tags.

23. (Original) Method according to one of the preceding claims, further characterized in that matrix-assisted laser desorption/ionization mass spectrometry (MALDI) is conducted in f).

24. (Original) Kit for conducting the method according to claim 1, containing a sample holder for a mass spectrometer, which is modified in such a way that randomly selectable portions of a genome are immobilized on the latter, and/or probe libraries, with which the DNA immobilized on the sample holder is analyzed by mass spectrometer and/or other chemicals, solvents and/or adjuvants, as well as, optionally, instructions for use.